

**Fig. 1**

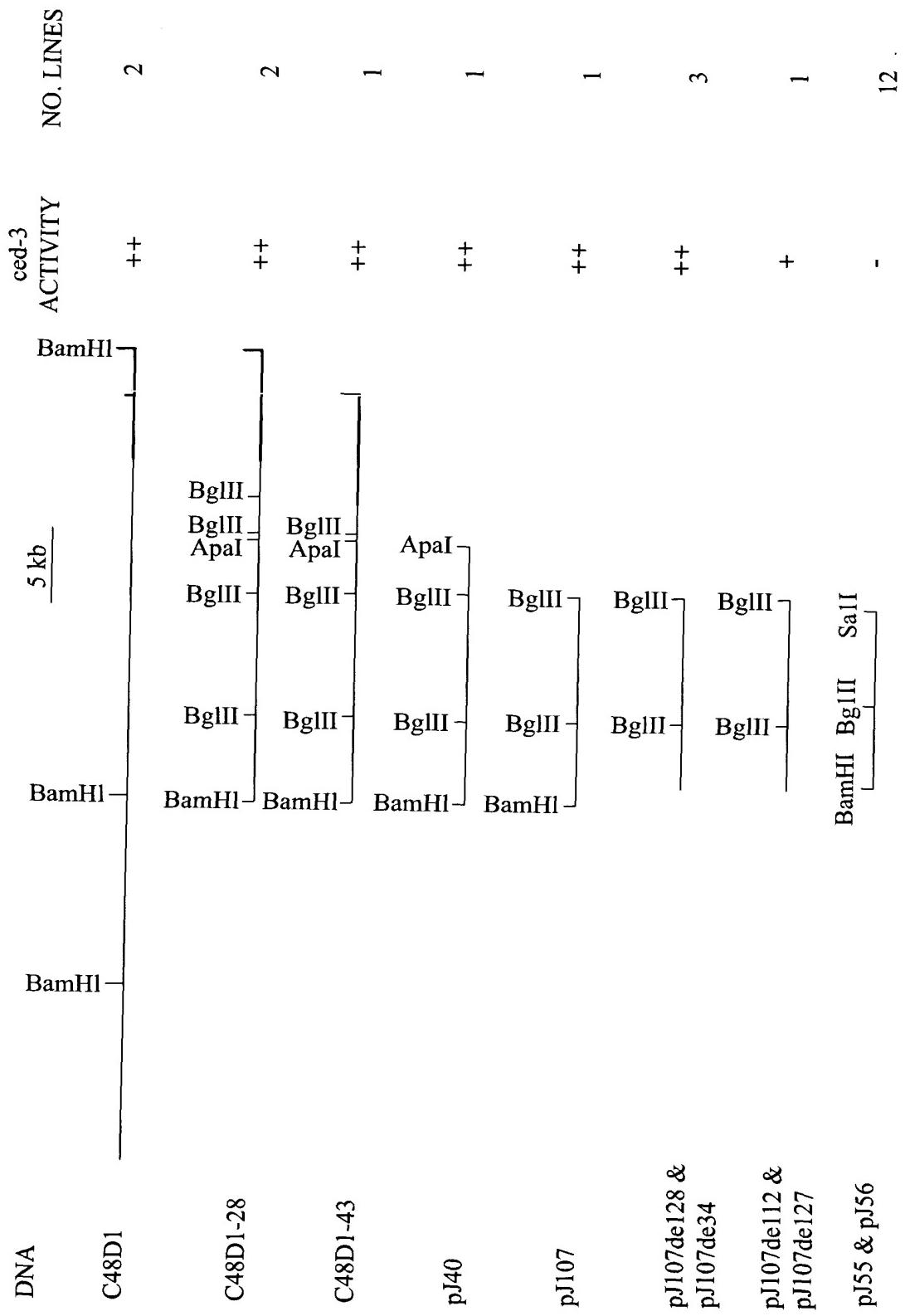


Fig. 2

## *ced-3* Genomic Sequence

AGATCTGAAATAAGGTGATAAAATTAAATAAGTGTATTCTGAGGAAATTGACTGT  
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
TTAGCACAAATTAAATCTGTTCAGAAAAAAAGTCCAGTTCTAGATTTCCGTCTTA  
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
TTGTCGAATTAAATATCCCTATTATCACTTTCATGCTCATCCTCGAGCGGCACGTCTC  
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
AAAGAATTGTGAGAGCAAACGCGCTCCCATTGACCTCACACTCAGCCGCAAAACAAAC  
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240  
GTTCGAACATTCTGTGTTGCTCCTTCCGTTATCTTGAGTCATCTTGTGCGTT  
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
TTTCCTTGTCTTTGTTGAACGTGTTGCTAAGCAATTATTACATCAATTGAAGAAAA  
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
GGCTCGCCGATTTATTGTTGCCAGAAAGATTCTGAGATTCTCGAAGTCGATTTATAATA  
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
TTAACCTGGTTTTGCATTGTTCGTTAAAAAAACCACTGTTATGTGAAAACGA  
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480  
TAGTTACTAATAAAACTACTTTAACCTTACCTTACCTCACCGCTCCGTGTTCATG  
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540  
GCTCATAGATTCGATACTCAAATCCAAAATAATTACGAGGGCAATTATGTGAAA  
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600  
CAAAAACAATCCTAAGATTCACATGTTGACCTCTCCGGCACCTCTTCCTTAGCCCC  
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660  
ACCACTCCATCACCTCTTGGCGGTGTTCTCGAAACCCACTTAGGAAAGCAGTGTGTAT  
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720  
CTCATTGGTATGCTCTTCGATTTATAGCTCTTGTGCAATTCAATGCTTAAAC  
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 760  
AATCCAAATCGCATTATATTGTGCATGGAGGCAAATGACGGGGTGGATCTAGATGA  
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
GATCAGGAGCTTCAGGGTAAACGCCGGTCATTTGTACCACATTCTCATCTTCCT  
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900  
GTCGTCTTGGTATCCTCAACTGTCCGGTTGTTTGTGCGTACACTCTCCGTGATGC  
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 960  
CACCTGTCCTCGTCTCAATTATCGTTAGAAATGTGAACTGTCCAGATGGGTGACTCATA  
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
TTGCTGCTGCTACAATCCACTTCTTCTCATCGGCAGTCTACGAGCCCATCATAAAC  
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080  
TTTTTTCCGCAAATTGCAATAAACCGGCAAAACTTCTCCAAATTGTTACGCAA  
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140  
TATATACAATCCATAAGAATATCTCTCAATGTTATGATTCTCGCAGCCTTCTCT  
1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
TCGTGTGCTAACATCTTATTTATAATTCCGCTAAATTCCGATTTGAGTATTA  
1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
ATTATCGTAAAATTATCATAATAGCACCAGAAACTACTAAAATGGTAAAAGCTCCTT  
1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320

### **Repeat 1**

```

=====
TAAATCGGCTCGACATTATCGTATTAAGGAATCACAAAATTCTGAGAATGCGTACTGC
1321 -----+-----+-----+-----+-----+-----+-----+ 1380

=====
AACATATTGACGGCAAAATATCTCGTAGCGAAAACACTACAGTAATTCTTTAAATGACTAC
1381 -----+-----+-----+-----+-----+-----+-----+ 1440

```

Fig. 3

◎ 9 月 13 日 星期五

Repeat 1

```

=====
> TGTAGCGCTTGTGTCGATTACGGGCTCAATTTGAAAATAATTTTTTCGAATT
=====
1441 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1500
=====
TGATAACCGTAAATCGTCACAACGCTACAGTAGTCATTARAGGATTACTGTAGTTCTA
1501 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1560
GCTACGAGATATTTGCGCGCAAATATGACTGTAATACGCATTCTGAATTTGTGTT
1561 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1620
TCCGTAATAATTCACAAGATTTGGCATTCCACTTAAAGGCGCACAGGATTATTCCA
1621 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1680
ATGGGTCTCGGCACGCAAAAGTTGATAGACTTTAAATTCTCCTTGCATTTTAATTC
1681 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1740
AATTACTAAAATTTCGTAATTTCTGTTAAAATTTAAAATCAGTTTCTAATATT
1741 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1800
TTCCAGGCTGACAAACAGAAACAAAAACACAACAAACATTAAAATCAGTTTCAAAT
1801 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1860
TAAAAAATAACGATTCTCATGAAAATTGTGTTTATGTTGCGAAAATAAGAGAACT
1861 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1920
GATTCAAAACAATTAAACAAAAAAACCCCCAAATCGCCAGAAATCAAGATAAAAAA
1921 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 1980
TTCAAGAGGGTCAAAATTTCCGATTTACTGACTTCACCTTTTCTGTAGTCAGT
1981 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2040
GCAGTTGTTGGAGTTTGACGAAAATAGGAAAAAATCGATAAAAATTACTCAAATCG
2041 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2100
AGCTGAATTTGAGGACAATGTTAAAAAAAAACACTATTTCACAATAATTCACTCAT
2101 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2160

-----
TTTCAGACTAAATCGAAAATCAAATCGTACTCTGACTACGGGTCAAGAGAGGTCAACC
-----
2161 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2220
ATCAGCCGAAGATGATGCGTCAAGATAGAAGGAGCTGCTAGAGAGGAACATTATGATGT
2221 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2280
      M   M   R   Q   D   R   R   S   L   L   E   R   N   I   M   M   F
      1           10
      T (n1040)
      |
      TCTCTAGTCATCTAAAGTCGATGAAATTCTCGAAGTTCTCATCGCAAAACAAGTGTGA
2281 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2340
      S   S   H   L   K   V   D   E   I   L   E   V   L   I   A   K   Q   V   L   N
      20          30
      | intron 1
      ATAGTGATAATGGAGATATGATTAATGTGAGTTTAATCGAATAATAATTTAAAAAAA
2341 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2400
      S   D   N   G   D   M   I   N
      40
      |
      AATTGATAATATAAGAATATTTGCAGTCATGTGGAACGGTTCGCGAGAAGAGACGGG
2401 - + - + - + - + - + - + - + - + - + - + - + - + - + - + 2460
      S   C   G   T   V   R   E   K   R   R   E
      50
  
```

Fig. 3 (cont.)

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A(n718)

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AGATCGTAAAGCAGTGCAACGACGGGGAGATGTGGCGTCGACGCCTTTATGATGCTC
2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
I V K A V Q R R G D V A F D A F Y D A L
       60                      70

| intron 2
TTCGCTCTACGGGACACGAAGGACTTGCTGAAGTTCTTGAACCTCTGCCAGATCGTAGG
2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+
R S T G H E G L A E V L E P L A R S
       80                      90

TTTTAAAGTTCGCGCAAAGCAAGGGCTCACGGAAAAAGAGGGGATCGTAATTT
2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640
GCAACCCACCAGGACGGTTTCTCCGAAAATCGAAATTATGCACCTTCCAAATAT
2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
TTGAAGTGAAATATTTTACTGAAAGCTCGAGTGATTATTATTTAACACTA
2701 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2760
ATTTCTGGCGCAAAGGCCATTTGTAGATTGCCGAAAATCTGTCACACACACAC
2761 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2820
ACACACATCTCCTCAAATATCCCTTTCCAGTGTGACTCGAATGCTGTCGAATTG
2821 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2880
V D S N A V E F E
       100

GTGTCCAATGTCACCGGAAAGCCATCGTCGGAGCCGCGCATTGAGCCCCGCCGGCTACAC
2881 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2940
C P M S P A S H R R S R A L S P A G Y T
       110                      120

TTCACCGACCGAGTTCACCGTGACAGCGTCTTCAGTGTCACTCATTCTTATCA
2941 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 3000
S P T R V H R D S V S S V S S F T S Y Q
       130                      140

GGATATCTACTCAAGAGCAAGAGATCTCGTTCTCGATCGCGTGCACATTCAATCGGATCG
3001 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 3060
D I Y S R A R S R S R S R A L H S S D R
       150 1                      60

| intron 3
ACACAATTATTCATCTCCTCCAGTCACGCATTCAGCCAACTTGTATGTTGATGCG
3061 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 3120
H N Y S S P P V N A F P S Q P S
       170

Repeat 1
=====
AACACTAAATTCTGAGAATGCGCATTACTAACATATTGACGCGCAAATATCTCGTAGC
3121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 3180
=====

GAAAAATACTGAAACCTTAAATGACTATTGTAGTGTGATTTACGGGCTCGATTTCG
3181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 3240
=====
```

**Fig. 3 (cont.)**

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==>  
AAACGAATATATGCTCGAATTGTGACAACGAATTTAATTGTCATTTGTGTTTCTT  
3241 -----+-----+-----+-----+-----+ 3300

Repeat 1

<=====  
TTGATATTTTGATCAATTAATAAATTATTCCTGAAACAGACACCAGCGCTACAGTACT  
3301 -----+-----+-----+-----+-----+-----+ 3360

=====  
CTTTAAAGAGTTACAGTAGTTTCGCTTCAGATATTTGAAAAGAATTTAACATTT  
3361 -----+-----+-----+-----+-----+-----+ 3420

=====  
TGAAAAAAAATCATCTAACATGTGCCAAACGCTTTCAAGTTCGCAGATTTTGA  
3421 -----+-----+-----+-----+-----+ 3480

Repeat 2

=====  
TTTTTTCATCAAGATATGCTTATTAAACACATATAATTATCATTAAATGTGAATTTCTG  
3481 -----+-----+-----+-----+-----+-----+ 3540

=====  
TAGAAATTTGGGCTTTCTAGTATGCTCTACTTTGAAATTGCTCAACGAAAAAA  
3541 -----+-----+-----+-----+-----+-----+ 3600

=====  
TCATGTGGTTGTTCATATGAATGACAAAAATAGCAATTTTATATATTTCCCCTAT  
3601 -----+-----+-----+-----+-----+-----+ 3660

=====  
TCATGTTGTGCAGAAAATAGTAAAAAGCGCATGCATTTGACATTTTACATCGA  
3661 -----+-----+-----+-----+-----+-----+ 3720

=====>  
ACGACAGCTCACCCACATGCTGAAGACGAGAGACGCGGAGAAATACCACACATTTCT  
3721 -----+-----+-----+-----+-----+-----+ 3780

Repeat 2

<=====  
GCGTCTCTCGTCTTCAGCATGTGAAATGGATCTGGTCATGTAAGAAAATGCGAATA  
3781 -----+-----+-----+-----+-----+-----+ 3840

=====  
ATGTAAAAAATGCATGCGTTTTTACACTTTCTGCACAAATGAATAGGGGGAAAATGT  
3841 -----+-----+-----+-----+-----+-----+ 3900

=====  
ATTAAAATACATTTTGATTTTCAACATCACATGATTAACCCATTATTTTCGTT  
3901 -----+-----+-----+-----+-----+-----+ 3960

=====  
GAGCAACTAAAAAGTAGAGAATATTAGAGCGAAAACCAAAATTCTCAAGATATTACC  
3961 -----+-----+-----+-----+-----+-----+ 4020

=====  
TTTATTGATAATTATAGATGTTAATAAGCATATCTGAATGAAAGTCAGCAAAATATGT  
4021 -----+-----+-----+-----+-----+-----+ 4080

Fig. 3 (cont.)

4081 -----+-----+-----+-----+-----+-----+ 4140  
 TTTTGCACTTCTACATCACATGAATGTAGAAAATTAAAAGGAAATCAAATTCTA  
 4141 -----+-----+-----+-----+-----+-----+ 4200  
 GAGGATATAATTGAATGAAACATTGCAGAAATTAAAATGTGCGAACGTCAAAAAAGAGGA  
 4201 -----+-----+-----+-----+-----+-----+ 4260

AATTTGGGTATCAAATCGATCCTAAACCAACACATTCAGCATCCGCCACTCTTCAT  
 4261 -----+-----+-----+-----+-----+-----+ 4320  
 S A N S S F  
 180

TCACCGGATGCTCTCTCGGATACAGTTCAAGTCGTAATCGCTCATTAGCAAAGCTT  
 4321 -----+-----+-----+-----+-----+-----+ 4380  
 T G C S S L G Y S S S R N R S F S K A S  
 190 200

CTGGACCAACTCAATACATATTCCATGAAGAGGGATATGAACCTTGTGATGCACCAACCA  
 4381 -----+-----+-----+-----+-----+-----+ 4440  
 G P T Q Y I F H E E D M N F V D A P T I  
 210 220

TAAGCCGTTTTCGACGAGAAAACCATGTACAGAAACTTCTCGAGTCCTCGTGGATGT  
 4441 -----+-----+-----+-----+-----+-----+ 4500  
 S R V F D E K T M Y R N F S S P R G M C  
 230 240

GCCTCATCATAATAATGAACACTTGGAGCAGATGCCAACACGGAATGGTACCAAGGCCG  
 4501 -----+-----+-----+-----+-----+-----+ 4560  
 L I I N N E H F E Q M P T R N G T K A D  
 250 260

ACAAGGACAATCTTACCAATTGTTCAAGATGCATGGCTATACGGTTATTGCAAGGACA  
 4561 -----+-----+-----+-----+-----+-----+ 4620  
 K D N L T N L F R C M G Y T V I C K D N  
 270 280

| intron 4  
 ATCTGACGGGAAGGGTACGGCGAAATTATATTACCCAAACGCGAAATTGCCATTGCG  
 4621 -----+-----+-----+-----+-----+-----+ 4680  
 L T G R

Repeat 3  
 =====>

CCGAAAATGTGGCCCGGTCTGACACGACAATTGTGTTAAATGCAAAATGTATAAT  
 4681 -----+-----+-----+-----+-----+-----+ 4740  
 TTTGCAAAAACAAAATTGAACTTCCCGCAGAAATTGATTACCTAGTTGCGAAATTTC  
 4741 -----+-----+-----+-----+-----+-----+ 4800  
 GTTTTTCCGGCTACATTATGTGTTTTCTTAGTTTCTATAATATTGATGTAAAAA  
 4801 -----+-----+-----+-----+-----+-----+ 4860  
 ACCGTTGTAAATTTCAGACAATTCCGCATACAAACTGATAGCACGAAATCAATT  
 4861 -----+-----+-----+-----+-----+-----+ 4920  
 TTCTGAATTTCAAAATTATCCAAAATGCAACATTAAATTGTGAAATTGGCAAAC  
 4921 -----+-----+-----+-----+-----+-----+ 4980

Fig. 3 (cont.)

GGTGTTCATGAAATGTATTTAAAAACTTAAAAACCACTCCGAAAAGCAATAA  
 4981 -----+-----+-----+-----+-----+-----+-----+ 5040  
 AAATCAAACACGTACAATTCAAATTCAAAGTTATTCATCCGATTGTTATTTG  
 5041 -----+-----+-----+-----+-----+-----+-----+ 5100  
 CAAAATTGAAAAATCATGAAGGATTAGAAAAGTTATAACATTCTAGATT  
 5101 -----+-----+-----+-----+-----+-----+-----+ 5160  
 TCAAAATTCTAACAAATCGAGAAAAGAGAATGAAAATCGATTAAAATATCC  
 5161 -----+-----+-----+-----+-----+-----+-----+ 5220

Repeat 3

<=====

ACAGCTTCGAGAGTTGAAATTACAGTACTCCTTAAGGCACACCCATTGCATTGG  
 5221 -----+-----+-----+-----+-----+-----+-----+ 5280

=====

ACCAAAAATTGTCGTGTCGAGACCAGGTACCGTAGTTTGTCGCAAAATTGCACCAT  
 5281 -----+-----+-----+-----+-----+-----+-----+ 5340  
 TGGACAATAAACCTCTAATCACCAAAAGTAAATTGAAATCTCGAAAAGCCAAAA  
 5341 -----+-----+-----+-----+-----+-----+-----+ 5400  
 ATTCAAAAAAAAGTCGAATTCGATTTTTGGTTTTGGTCCAAAACCAAAA  
 5401 -----+-----+-----+-----+-----+-----+-----+ 5460  
 AAATCAATTCTGAAAATACCAAAAGAAACCGAAAAATTCCCAGCCTGTTCT  
 5461 -----+-----+-----+-----+-----+-----+-----+ 5520

|

AATGTAAACTGATATTAAATTCCAGGGAATGCTCCTGACAATTGAGACTTGCCAAAC  
 5521 -----+-----+-----+-----+-----+-----+-----+ 5580  
 G M L L T I R D F A K H  
 290 300

ACGAATCACACGGAGATTCTGCGATACTCGTGATTCTACACGGAGAAGAGAATGTGA  
 5581 -----+-----+-----+-----+-----+-----+-----+ 5640  
 E S H G D S A I L V I L S H G E E N V I  
 310 320

TTATTGGAGTTGATGATACCGATTAGTACACACGGAGATATGATCTCTAACCGGG  
 5641 -----+-----+-----+-----+-----+-----+-----+  
 I G V D D I P I S T H E I Y D L L N A A  
 330 340

A(n2433)  
| | intron 5

CAAATGCTCCCCGTCTGGCGAATAAGCCAAAATGTTTGTGCAGGCTGTCGAGGCG  
 5701 -----+-----+-----+-----+-----+-----+-----+ 5760  
 N A P R L A N K P K I V F V Q A C R G E  
 350 360

|

GTTCGTTTTATTTAATTTAATATAAATTTAAATAATTCAATTTCAGAACGTC  
 5761 -----+-----+-----+-----+-----+-----+-----+ 5820  
 R R

GTGACAATGGATTCCAGTCTGGATTCTGCGACGGAGTTCCCTGCATTCTCGTCGTG  
 5821 -----+-----+-----+-----+-----+-----+-----+ 5880  
 D N G F P V L D S V D G V P A F L R R G  
 370 380

Fig. 3 (cont.)

T (n1165)

```

GATGGGACAATCGAGACGGGCCATTGTTCAATTTCTTGGATGTGTGCGGCCGCAAGTTC
5881 -----+-----+-----+-----+-----+-----+-----+-----+-----+
W D N R D G P L F N F L G C V R P Q V Q
390          400

```

| intron 6

```

AGGTTGCAATTAAATTCTTGAATGAGAATATTCCCTCAAAAATCTAAAATAGATTTT
5941 -----+-----+-----+-----+-----+-----+-----+-----+
ATTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTGTGATAAAATGAC
6001 -----+-----+-----+-----+-----+-----+-----+

```

Repeat 4

```

=====
AAACCAATCAGCATCGTCGATCTCCGCCACTTCATCGGATTGGTTGAAAGTGGCGGA
6061 -----+-----+-----+-----+-----+-----+-----+

```

===== >

```

GTGAATTGCTGATTGGTCGCAGTTTAGAGGAAATTAAAAATCGCCTTTCGA
6121 -----+-----+-----+-----+-----+-----+-----+
AAATTAAAAATTGATTTCATTTTGAAATTCCGATTATTATATTCTTT
6181 -----+-----+-----+-----+-----+-----+

```

A (n717)

```

GGAGCGAAAGCCCCGTCTGTAAACATTAAATGATAATTAATAAATTGGCAGCAA
6241 -----+-----+-----+-----+-----+-----+-----+
Q

```

T (n1949)

```

GTGTGGAGAAAGAACGCCGAGCCAAGCTGACATTCTGATTGATACGCAACGACAGCTCAA
6301 -----+-----+-----+-----+-----+-----+-----+
V W R K K P S Q A D I L I R Y A T T A Q
410          420

```

A (n1286)

```

TATGTTCTGGAGAAACAGTGCTCGTGGATCATGGTCATTCAAGCCGTCTGTGAAGTG
6361 -----+-----+-----+-----+-----+-----+-----+
Y V S W R N S A R G S W F I Q A V C E V
430          440

```

T (n1129, n1164)

```

TTCTCGACACACGCAAAGGATATGGATGTTGAGCTGCTGACTGAAGTCAATAAGAAG
6421 -----+-----+-----+-----+-----+-----+-----+
F S T H A K D M D V V E L L T E V N K K
450          460

```

T (n2430)   A (n2426)

```

GTCGCTTGTGGATTCAGACATCACAGGGATCGAATATTTGAAACAGATGCCAGAGGTA
6481 -----+-----+-----+-----+-----+-----+-----+-----+
V A C G F Q T S Q G S N I L K Q M P E
470          480

```

| | intron 7

Fig. 3 (cont.)

Repeat 5

```

=====
CTTGAACAAACAATGCATGTCTAAGGACACAGAAAAATAGGCAGAGGCTCCT
6541 -----+-----+-----+-----+-----+-----+ 6600

=====>
TTGCAAGCCTGCCGCGCGTCAACCTAGAATTAGTTAGCTAAAATGATTGATTT
6601 -----+-----+-----+-----+-----+-----+ 6660
GAATATTTATGCTAATTTTGCCTAAATTTGAAATAGTCACTATTTATCGGGTTT
6661 -----+-----+-----+-----+-----+-----+ 6720
CCAGTAAAAAAATGTTATTAGCCATTGGATTACTGAAAACGAAAATTGTAGTTTC
6721 -----+-----+-----+-----+-----+-----+ 6780
AACGAAATTATCGATTTAAATGTAACGAAAATTACATCAACCATAA
6781 -----+-----+-----+-----+-----+-----+ 6840
GCATTAAAGCCAAATTGTTAECTCATTAAAAATTCAAAGTTGTCCACGAGTATT
6841 -----+-----+-----+-----+-----+-----+ 6900

```

Repeat 5

```

<=====
ACACGGTTGGCGCGCGCAAGTTGCAAAACGACGCTCCGCCTTTCTGTGCGGCTT
6901 -----+-----+-----+-----+-----+-----+ 6960

=====
GAAAACAAGGGATCGTTAGATTTCCCCAAATTAAATTCAAGATGACATC
6961 -----+-----+-----+-----+-----+-----+ 7020
|          |          |
|          T(n1163)
M T S

CCGCCTGCTCAAAAGTTCTACTTTGCCGGAAGCACGAAACTCTGCCGTCTAAAATTC
7021 -----+-----+-----+-----+-----+-----+ 7080
R L L K K F Y F W P E A R N S A V *
490          500
ACTCGTGATTCAATTGCCAATTGATAATTGCTGTATCTTCTCCCCAGTTCTTTCGC
7081 -----+-----+-----+-----+-----+-----+ 7140
CCAATTAGTTAAACCATGTGTATATTGTTATCCTATACTCATTCACTTTATCATTCT
7141 -----+-----+-----+-----+-----+-----+ 7200
ATCATTCTCTCCCATTTCACACATTCCATTCTCTACGATAATCTAAAATTATGAC
7201 -----+-----+-----+-----+-----+-----+ 7260
GTTTGTGTCGAACGCATAATAATTAAACTCGTTGAATTGATTAGTTGTTGT
7261 -----+-----+-----+-----+-----+-----+ 7320
GCCAGTATATGTACTATGCTCTATCAACAAAATAGTTCATAGATCATCACC
7321 -----+-----+-----+-----+-----+-----+ 7380
CCAACCCCACCAACCTACCGTACCATATTCTATTGGCCGGAAATCAATTGATTAATT
7381 -----+-----+-----+-----+-----+-----+ 7440
TTAACCTATTTTCCACAAAAATCTAATATTGAATTAAACGAATAGCATTCCATC
7441 -----+-----+-----+-----+-----+-----+ 7500
TCTCCCGTGCCGAATGCCCTCCGGCTTTAAAGTTGGAACATTGGCAATTATGTAT
7501 -----+-----+-----+-----+-----+-----+ 7560
AAATTGTAGGTCCCCCCCACATCTTCCGCCATCATCTCAAATTGCATTTTTCG
7561 -----+-----+-----+-----+-----+-----+ 7620
CCGTGATATCCGATTCTGGTCAGCAAAGATCT
7621 -----+-----+-----+-----+-----+-----+ 7653

```

Fig. 3 (cont.)

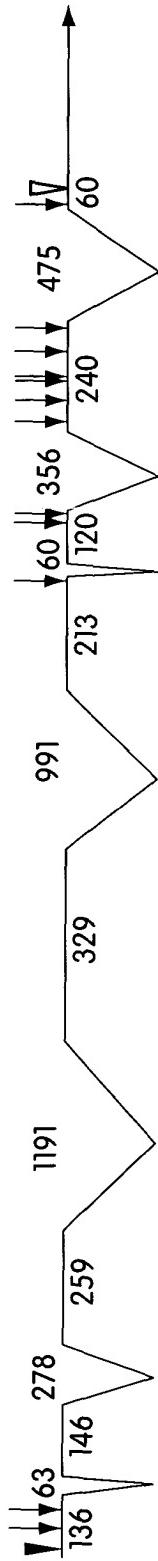


Fig. 4A

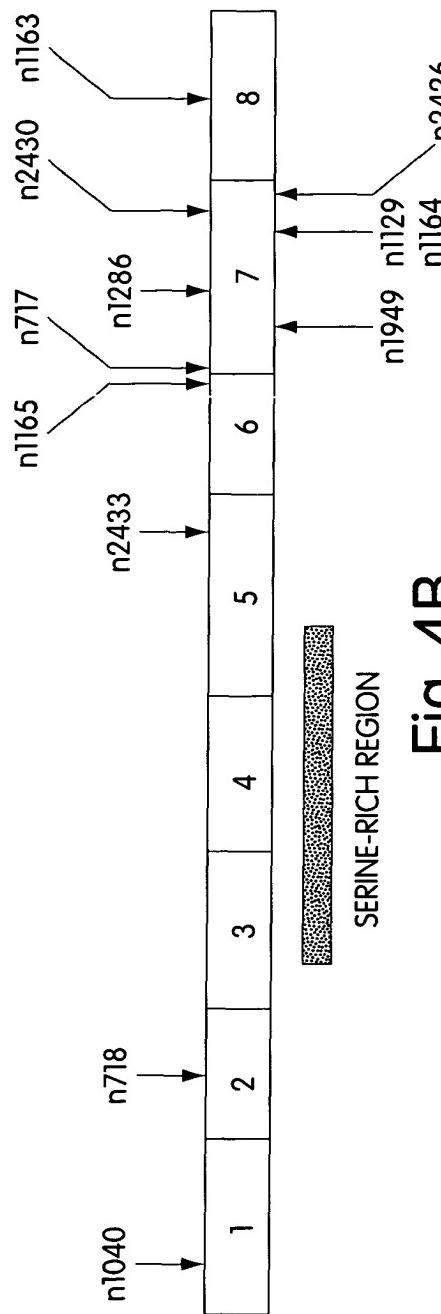


Fig. 4B

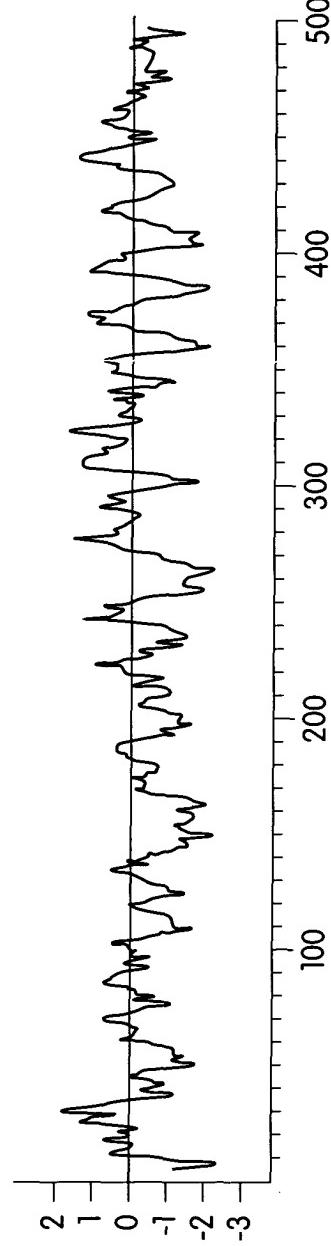


Fig. 5

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Alignment of ced-3 and Human Interleukin -1 $\beta$  convertase

ICE	1	MADKVLKEKRKLFIRSM....GEGTINGLLDELLQTRVLNKEEMEKVKRE .. .:: .:  .. . .::: :  ...   ..: .. .
Ced-3	1	...MMRQDRRSLLERNIMMFSSHLKVDEILEVLIAKQVLNSDNGDMIN.S ↓ F
BGAFAQ		=====
PBA		=====
	47	NATVMDKTRALIDSVIPKGAAQACQ.ICITYICEEDSYLAGTLGLSADQTS : .:  .:...  .. .   : : .. :...   : :   ..
	47	CGTVREKRREIVKAVQRPGDVAFDAFYDALRSTGHHEGLAEVLEPLARSVD ↓ R
BFAFAQ		=====
PBA		=====
	96	GNYLNMQ.....DSQGVLSSF..... :  :::
	97	SNAVEFEC <u>CPMS</u> PASHRRSR <u>ALSPAGYTS</u> PTRVHRDSVSSVSSFTSYODIY serine-rich region
BGAFAQ		=====
PBA		=====
	112	.....PAPQAVQDNPAMPTSSGSEGNVKLCSE  :.. .... . .:   . . . . .  .
	147	<u>SRARSRSRSRALHSSDRHNYSSPPVNAFPSSOPSSANSSFTGCSSLGYSSS</u>
BGAFAQ		=====
PBA		==
	140	EAQRIWKQKSAEIYPIMDK.....SSRTRLAL .... ....  . : . .   . .
	197	<u>RNRSFSKASGPTQYIFHEEDMNFDAPTISRVFDEKTMYRNFS</u> SSPRGMCL
BGAFAQ		=====

Fig. 6A

ICE 167 IICNEEFDSIPRRTGAEV DITGMTLLQNLGY SVDVKKNL TASDMTTELE  
 || || .: :| | .|...| ..:| | .. :||. | .|.|||:..| ..:  
 Ced-3 247 IINNEHFEQM PTRNGTKADKDNL TNLFRCM GYTVICKDNLTGRGMLLTIR  
 BGAFQ ======  
  
 217 AFAHRPEHKTSDSTFLVFM SHGIREGICGKKHSEQVPDI. LQLNAIFNML  
 .||. .... :||.:||:||| ..|. | .|| : ..|:..|:  
 297 DFAKHESH.. GDSAILVILSHGEENVIIG..... VDDIPISTHEIYDLL  
 BGAFQ ======  
  
 active site autocleavage site  
 266 NTKNCPSLKD KPKVII IQACRGDSPGVW. FKDSVGSGNLSLPTTEEFE  
 |. |..|. :|||:::|||:...: .. . |||:.. ..: .. :: :  
 339 NAANAPRLANKPKIVFVQACRGERRDNGFPVLDSDGVPAFLRRGWDNRD  
 ↓  
 S  
 BGAFQ ======  
  
 315 DDAI..... KKAHIEKDFIAFCSSTPDNVSWRHPTMGSVFI  
 .. : :| .. |:: ..|:: |||:...|| |||  
 389 GPLFNFLGCVRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFI  
 ↓ stop ↓ stop  
  
 351 GRLIEHMQEYACSCDV EEIF.... RKVRF SFE QPDGRAQMPTT. ERVT. L  
 . :. | : ..| . |||:: :|| :|: ..|... : .. | .. | .:  
 439 QAVCEVFSTHAKMDV VELLTEVNKKVACGFQTSQGSNILKQMPEMTSRL  
 ↓ V ↓ V ↓ K ↓ F  
  
 395 TRCFYLFPGH\*.... 404  
 : ||::|:  
 489 LKKFYFWPEARNSAV 503

Fig. 6A (cont.)

## Alignment of Ced-3 and Murine NEDD-2

499 RNSAV 503  
169 PPT. . . 172

Fig. 6B

## Alignment of N-terminal regions of ced-3/ICE-related proteins

c. briggsae ced-3 MMRQDRWSLLERNLLEFSKQLQADLILLYLIAKQVNLNSDNGDVINSCTERDNEKEIVRAVQRGQDEAFDAFYDALRDTGHNDIADVLIMPLSR---PNPV  
ced-3 protein MMRQDRRSLLERNLIMMFTSHSLKVDELETLIAKQVNLNSDNGDMINSGCTVREKRREIVRAVQRPGDVAFDAFYDALRSTGHEGLAEVLEPLARSVDSSAV 100

C.vulgaris ced-3 M-----RAKEKQFINSV---SISTINGLDELLEK----RVLNQEEM----DKI  
Mouse ICE gw M-----ADKIL----ADKVL----KEKRKLFIKS---GEITINGLDELLOQT----RVLNKEEM----EKV  
Human ICE.GW M-----AD. II-----AD. II-----R. KRK.----V...G.....D.L.T.....VL.....V

Consensus M.....PMECPMSPPSERRSRALSPFQYASPTTVERDSISSSSFTSTYDQVYRSARSSSSRLQSSSDRATMSAA-TSFPSQPSANSSFTGGCASI LGYSSSSRN  
ced-3 protein EFECPMSPASERRSRALSPAGITSPTRVERDSVSSSSFTSYQD-IYSRARSRSSRS-RALHSSSDRATYSSPPVNAFPSPQSPSANSFTGGCSSLGYSSSSRN 198

C.vulgaris ced-3 STSRSSRPLETSDRHNTYSPS-NSFQSQPASANSFTGGCSSLGYSSSSRT  
Mouse ICE gw KLA---NITAMDKARDLCDENVSKXKGPOAQSQIFTYICNEDCYL  
Human ICE.GW KRE---NATVMDKTRALIDSVPKGAQACQCIITYICEEDSYL

Consensus ..E----.RAL.....I.....SY. ....S.SRS.R.L.SSDRHY.N.S...-..F.SQP.SANSSFTG.-SLGYSSSSR.

c. briggsae ced-3 RSFSKRTSAQSOQYIFHEEDWNYVDAPIIERYFDEKTYWYRFNFSSPRIGLCLTINNEHTEQMPPTNGTKLKDKNLTDNLTGRENLTIRSF  
ced-3 protein RFSKASAGPQYIIFHEEDWNYVDAPIIERYFDEKTYWYRFNFSSPRGMOLIINNEHTEQMPPTNGTKLKDNLTDNLTGRENLTIRDF 298  
C.vulgaris ced-3 RSYSKASASRSQYIIFHEEDWNYVDAPIIERYFDEKTYWYRFNFSSPRGLCLTINNEHTEQMPPTNGTKLKDNLTDNLTGRENLTIRDF  
Mouse ICE gw TFPGLGTGLKFCPLEKAQKLUKWNPS--EYI-PIMDKS-SRTR-LAIIIONTFQHLSPRVGAQYLREMKLLEDLGYTVKVRENLTALLEENKEKF  
Human ICE.GW TSSSGEGNVKLQCSLEEAQRMWKQSA--EYI-PIMDKS-SRTR-LAIIIONTFDTSIPRRTGAEVDTGWTMLQNQIYSDVRKLNLTSDMTTELEAF

Consensus RS.SK.S...QYIHEEDWN.VDAPII.RVFDEKTYWYRFNFSSPRGLCLTINNEHTEQMPPTNGTK.DKDN.TNLFRCMGYTV.CKDNLTDG.ML.TIR.E

c. briggsae ced-3 GRNDME-GDSAILVTLISRGEEVNTIG--VDDVS--VNVEIYDLINAANAPRILANKPFLVTVQACRG  
ced-3 protein AKHESE-GDSAILVTLISRGEEVNTIG--VDDIP--ISTHEIYDLINAANAPRILANKPFLVTVQACRG 360  
C.vulgaris ced-3 AKNETH-GDSAILVTLISRGEEVNTIG--VDDVS--VNVEIYDLINAANAPRILANKPFLVTVQACRG  
Mouse ICE gw AACPEEKTSDSTFLVTSISHGIOEGICGTTYSNEVSIDLKVDTIQOMMTNINCSELKDPKVIIQACRG  
Human ICE.GW AHRPEEKTSDSTFLVTSISHGIREGICGKHSSEQVDPDILQNLNAIFNMINTKNCPSLKUKPKVIIQACRG

Consensus A....H..CDSAIILVTLISRGEEVNTIG--VDDVS--.VNVEIYDLINAANAPRILANKPFLVTVQACRG

## Alignment of C-terminal regions of ced-3/ICE/NEJD-2 - related proteins

ICE C-terminus	DSPGVVV-	-	-	FIDSVG-	-	-	V
Mouse ICE C-ter	EKQGVNL-	-	-	LKDSTV-	-	-	D
C.briggsae C-ter	ERRDNGFP-	-	-	VLDSTDG-	-	-	
ced-3Cterminus	ERRDNGFP-	-	-	VLDSTDG-	-	-	RRGWDN
C.vulgaris C-terminus	ERRDVGFP-	-	-	VLDSTDG-	-	-	RRGWDN
nedd-2 protein.gw	MLTVQVITRS	QKCSSSKHEV	EVLDPPLGTS	FCSSLPPPLL	LYETDRGVVDQ		
Consensus	E.....	.....	.....	I D S V ..	.....	P ...	-----RG.D.
ICE C-terminus	SGNL---SIP	TTEEEF---D	DAIKKA-HIE	KDFIAFCSSST	PDNVSWRHEPT		
Mouse ICE C-ter	SEE---DFL	TDIAFE---D	DGIKKA-HIE	KDFIAFCSSST	PDNVSWRHEPV		
C.briggsae C-ter	RDG-PLFNFL	GCVRPQV--Q	QWWRKK-PSQ	ADMLIAYATT	AQYVSWRNSA		
ced-3Cterminus	RDG-PLFNFL	GCVRPQV--Q	QWWRKK-PSQ	ADMLIAYATT	AQYVSWRNSA	432	
C.vulgaris C-terminus	GDG-P--NFL	GCVRPQA--Q	QWWRKK-PSQ	ADMLIAYATT	AQYVSWRNSA		
nedd-2 protein.gw	QDGKRNHTQSP	GCEEDAGKE	ELMKRRLPTR	SDMICYACL	KGNAAAMRNTK		
Consensus	.DG. ....FL	GC.....	.....	K.-P. ....	D....YA.T	...VSWEIN..	
ICE C-terminus	<u>MGSVFTIGRLI</u>	<u>EHMOYIACSC</u>	<u>DVEELIFRAV</u>	<u>-RF</u>	<u>----SFE</u>	<u>QPDGCRQMP</u>	
Mouse ICE C-ter	RGSLLFTESLI	KHMKEYAWSC	DIEDIFRAV-	-RF	----SFE	QPERFLQMP	
C.briggsae C-ter	RGSWFTIQAVC	EVFSLHAKDM	DVVELLTENV	KKVA--CGFQ	TSQGSNLIKQ		
ced-3Cterminus	RGSWFTIQAVC	EVFSTHAKDM	DVVELLTENV	KKVA--CGFQ	TSQGSNLIKQ	480	
C.vulgaris C-terminus	RGSWFTIQAVC	EVFSLHAKDM	DVVELLTENV	KKVA--CGFQ	TSQGANLIKQ		
nedd-2 protein.gw	RGSWFTIEALT	QVTSERACDM	AVADDLIVWN	ALIKEREGYA	PCTEFERCKE		
Consensus	RGS.FL.A...	EVFS..A.	DM DV.E.L.M.	.....	GF.	...G....K.	
ICE C-terminus	T-ERVTLTR	CFYLFPGH	--	--	--	--	
Mouse ICE C-ter	A-DRVTLTK	RFYLFPGH	--	--	--	--	
C.briggsae C-ter	MPELTTSRLLK	KFYFWPEDRG	RNSAV				
ced-3Cterminus	MPEWTTSRLLK	KFYFWPEAR-	-NSAV	503			
C.vulgaris C-terminus	MPELTTSRLLK	KFYFWPEDRN	RSSAV				
nedd-2 protein.gw	MSEYCSTLICQ	QYXLFPG	--	-YPPT			
Consensus	M.E..S.L.K.	.FY..P.	....	....	....	....	

Fig. 6D

Lines

1	01	MMRQDRRSLLERNIMMFSSHLKVDEILEVLIAKQVLNSDNGDMINSCGTV	50
2		.....W.....LE...K.QA.L.D.....V....R.E	
3		TVSISLI..R.....M.....	
1	51	REKRREIVKAVQRPGDVAFDAFYDALRSTGHEGLAEVLEPLARSVDNAV	100
2		.DNEK.....R..E.....D...ND..D..M..S.P ..P.	
3			
1	101	EFECPMSPASHRRSRALSPAGYTSPTRVHR <u>D</u> <b>S</b> VSSVSSFTS_YQDIYSRA	149
2		PM.....S.....P .A.....I.....T...V....	
3		S	
1	150	RSRSR_SRALHSSDRHNYSSPPVNAFPSQPSSANSSFTGCSSLGYSSSRN	198
2		..S..S..P.Q.....M.AA_TS.....A.....	
3		T.....P..T.....V..S..S.Q..A.....S.....T	
1	199	RSFSKASGPTQYIFHEEDMNFDAPTISRVFDEKTMYRNFS <del>S</del> PRGMCLI	247
2		.....T.AQS.....Y.....H.....L...	
3		..Y.....AHS.....Y.....H.....T...L...	
1	248	INNEHFEQMPTRNGTKADKDNLTNLFRCMGYTICKDNLTGRGMLLTIRD	297
2		.....I.....E..S...S	
3		.....P....IS.....I.H.....M.....	
1	298	FAKHESHGDSAILVILSHGEENVIIGVDDIPISTHEIYDLLNAANAPRLA	347
2		.GRNDM.....VSVNV.....	
3		...N.T.....VSVNV....X.....	
1	348	NKPKIVFV <u>QACRGERRDNGFPVL</u> <b>D</b> SGVP AFLRRGWDNRDGPLNFLGC	397
2		....L.....SLI.....	
3		....L.....V.....LI.....KG... ....	
1	398	VRPQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST	447
2		.....M..A.....L	
3		....A.....A.....L	
1	448	HAKDMDVELLTEVNKKVACGFQTSQGSNILKQMPEMTSRLKKFYFWPE	497
2		.....L.....	
3		.....A.....L.....	
1	498	<u>ARN</u> _ SAV 503	
2		DRG..._...	
3		__D..RS...	

Fig. 7

09883243 - 062201

Interleukin-1 $\beta$  convertase cDNA sequence

1 AAAAGGAGAG AAAAGCCATG GCCGACAAGG TCCTGAAGGA GAAGAGAAAG  
 51 CTGTTTATCC GTTCCATGGG TGAAGGTACA ATAAATGGCT TACTGGATGA  
 101 ATTATTACAG ACAAGGGTGC TGAACAAGGA AGAGATGGAG AAAGTAAAAC  
 151 GTGAAAATGC TACAGTTATG GATAAGACCC GAGCTTGAT TGACTCCGTT  
 201 ATTCCGAAAG GGGCACAGGC ATGCCAAATT TGCATCACAT ACATTTGTGA  
 251 AGAAGACAGT TACCTGGCAG GGACGCTGGG ACTCTCAGCA GATCAAACAT  
 301 CTGGAAATTA CCTTAATATG CAAGACTCTC AAGGAGTACT TTCTTCCTTT  
 351 CCAGCTCCTC AGGCAGTGCA GGACAACCCA GCTATGCCA CATCCTCAGG  
 401 CTCAGAAGGG AATGTCAAGC TTTGCTCCCT AGAAGAAGCT CAAAGGATAT  
 451 GGAAACAAAA GTCGGCAGAG ATTTATCCAA TAATGGACAA GTCAAGCCGC  
 501 ACACGTCTTG CTCTCATTAT CTGCAATGAA GAATTTGACA GTATTCTAG  
 551 AAGAACTGGA GCTGAGGTTG ACATCACAGG CATGACAATG CTGCTACAAA  
 601 ATCTGGGTA CAGCGTAGAT GTGAAAAAAA ATCTCACTGC TTCGGACATG  
 651 ACTACAGAGC TGGAGGCATT TGCACACCGC CCAGAGCACA AGACCTCTGA  
 701 CAGCACGTTTC CTGGTGTCA TGTCTCATGG TATTCGGAA GGCATTTGTG  
 751 GGAAGAAACA CTCTGAGCAA GTCCCAGATA TACTACAAT CAATGCAATC  
 801 TTTAACATGT TGAATACCAA GAACTGCCA AGTTTGAAGG ACAAAACGAA  
 851 GGTGATCATC ATCCAGGCCT GCCGTGGTGA CAGCCCTGGT GTGGTGTGGT  
 901 TTAAAGATTG AGTAGGAGTT TCTGGAAACC TATCTTTACC AACTACAGAA  
 951 GAGTTGAGG ATGATGCTAT TAAGAAAGCC CACATAGAGA AGGATTTAT  
 1001 CGCTTCTGC TCTTCCACAC CAGATAATGT TTCTTGGAGA CATCCCACAA  
 1051 TGGGCTCTGT TTTTATTGGA AGACTCATTG AACATATGCA AGAATATGCC  
 1101 TGTTCTGTG ATGTGGAGGA AATTTCCGC AAGGTTCGAT TTTCATTGAA  
 1151 GCAGCCAGAT GGTAGAGCGC AGATGCCAC CACTGAAAGA GTGACTTTGA  
 1201 CAAGATGTTT CTACCTCTTC CCAGGACATT AAAATAAGGA AACTGTATGAA  
 1251 ATGTCTGCGG GCAGGAAGTG AAGAGATCGT TCTGTAAAAG GTTTTGGAA  
 1301 TTATGTCTGC TGAATAATAA ACTTTTTTG AAATAATAAA TCTGGTAGAA  
 1351 AAATGAAAAA AAAAAAAAAA AAA

Fig. 8

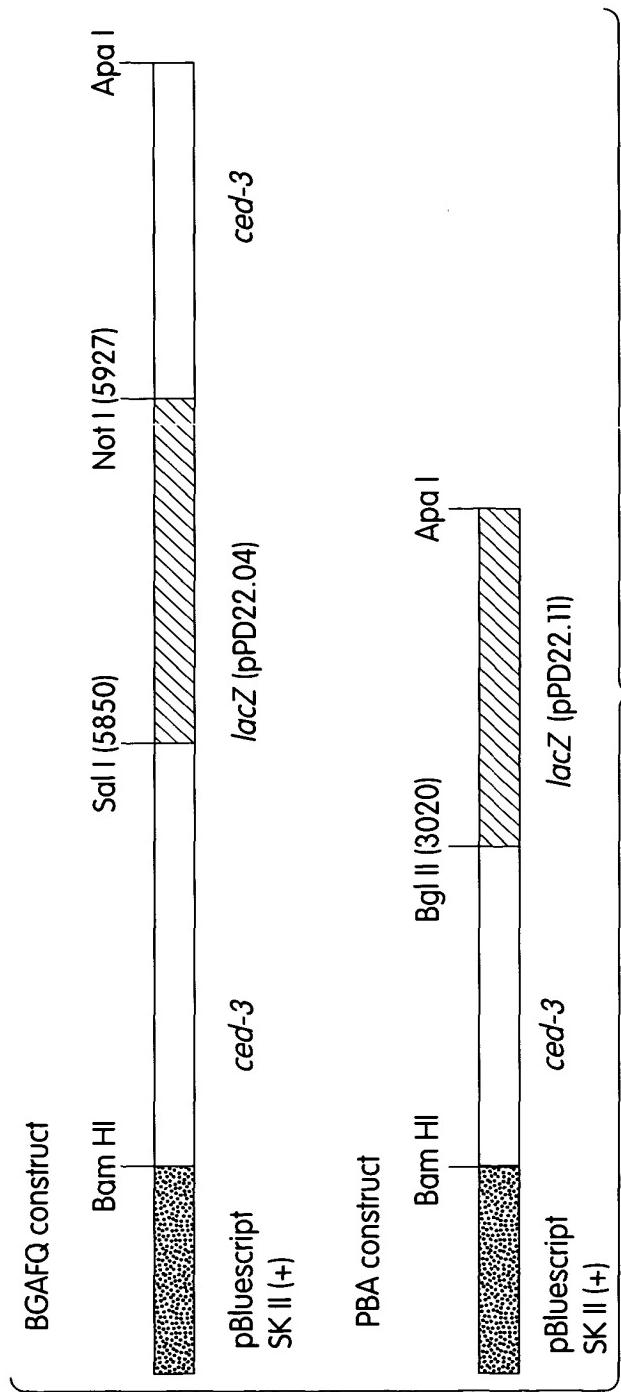


Fig.9A

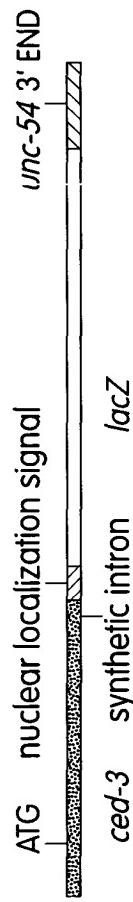


Fig. 9B

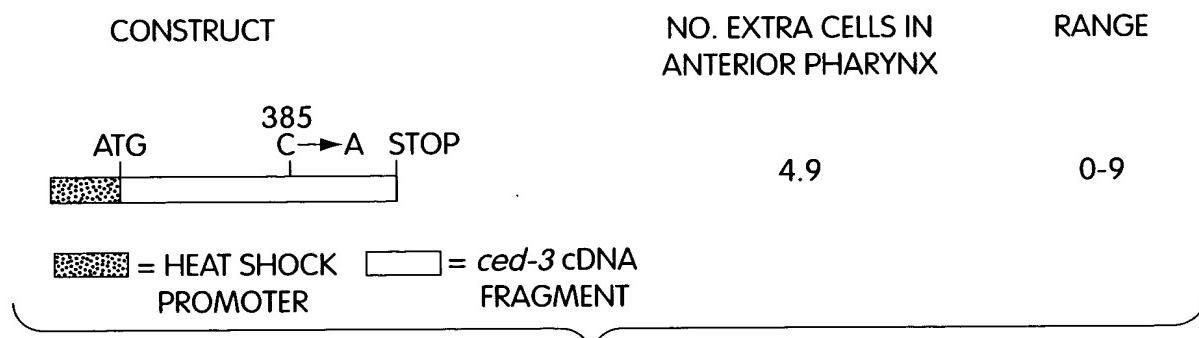


Fig. 10

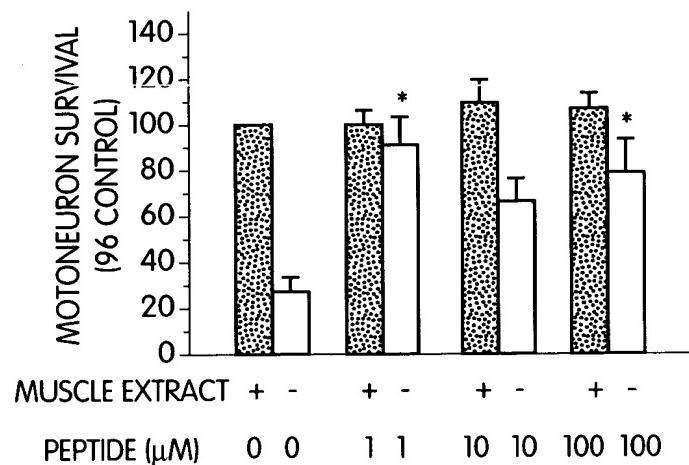


Fig. 11A

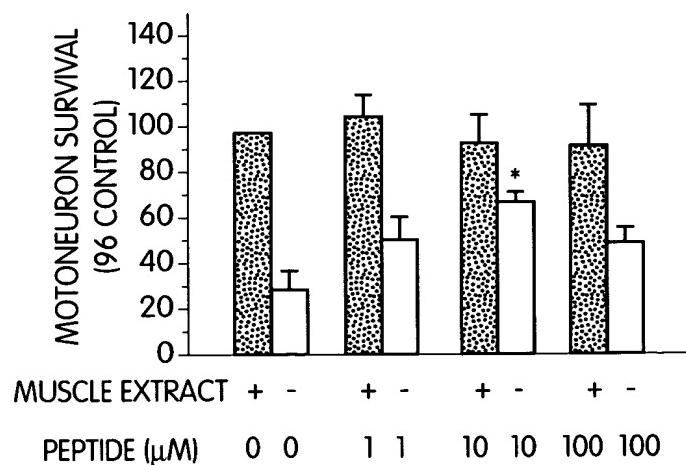


Fig. 11B

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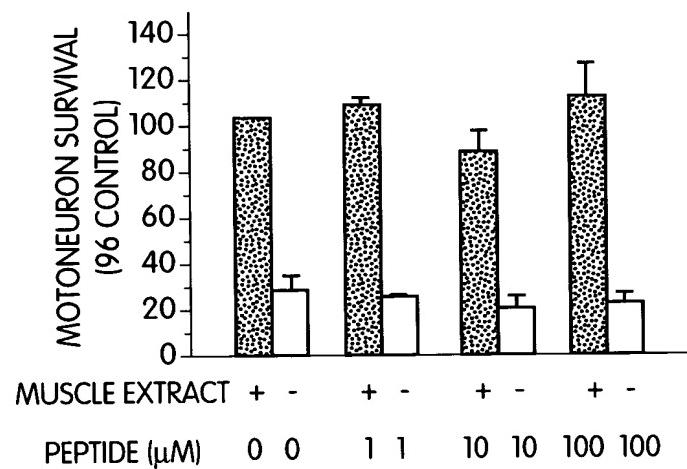


Fig. 11C

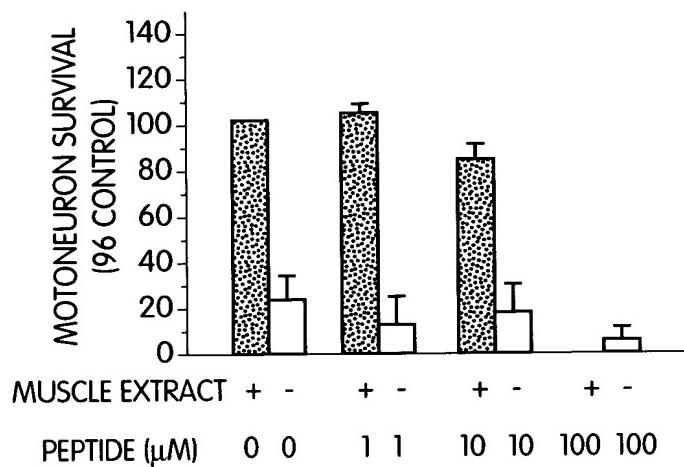


Fig. 11D

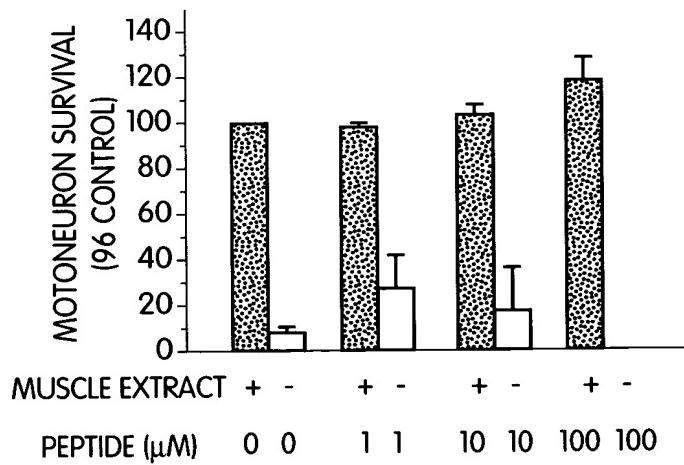


Fig. 11E

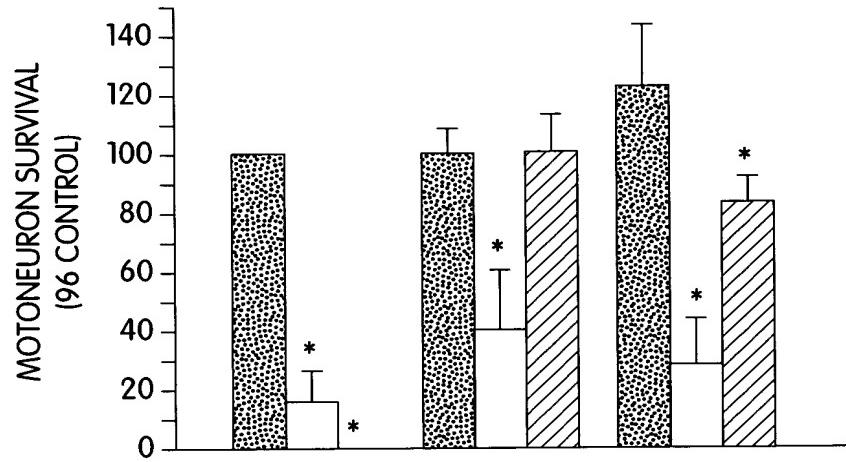


Fig. 12A

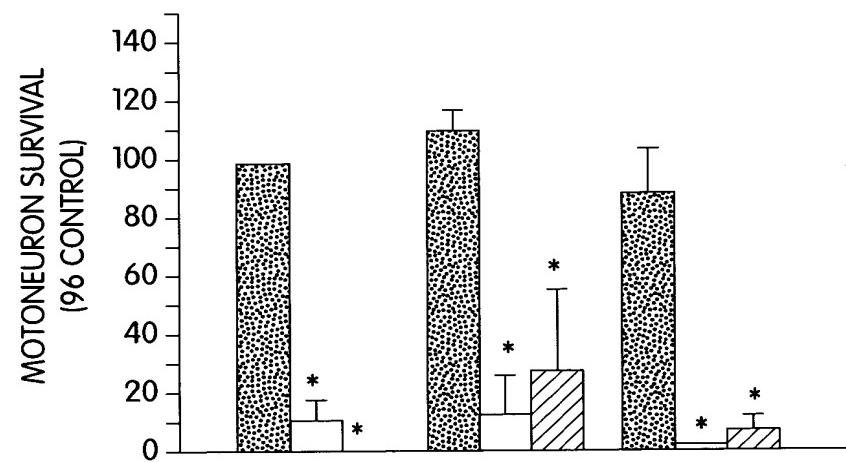


Fig. 12B

F02220 "E7223260

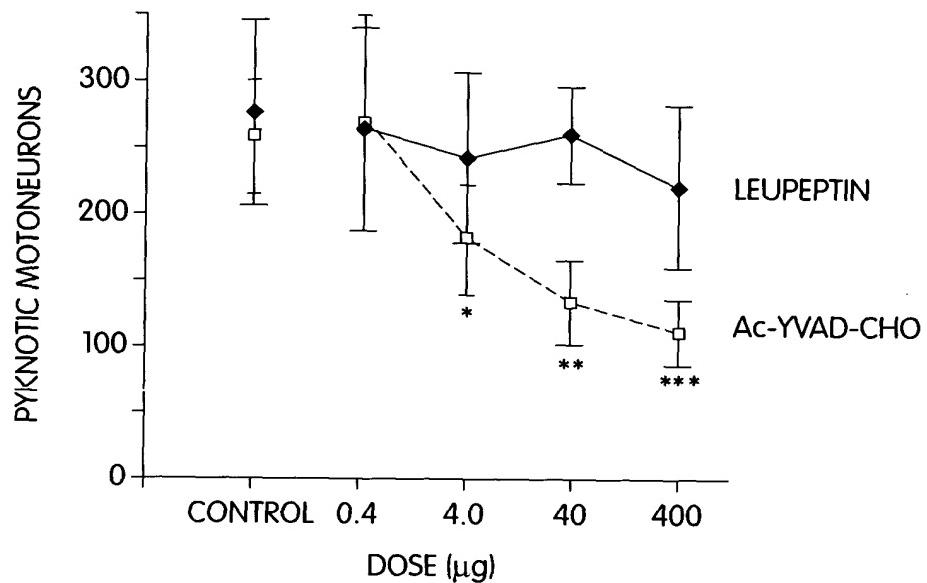


Fig. 13

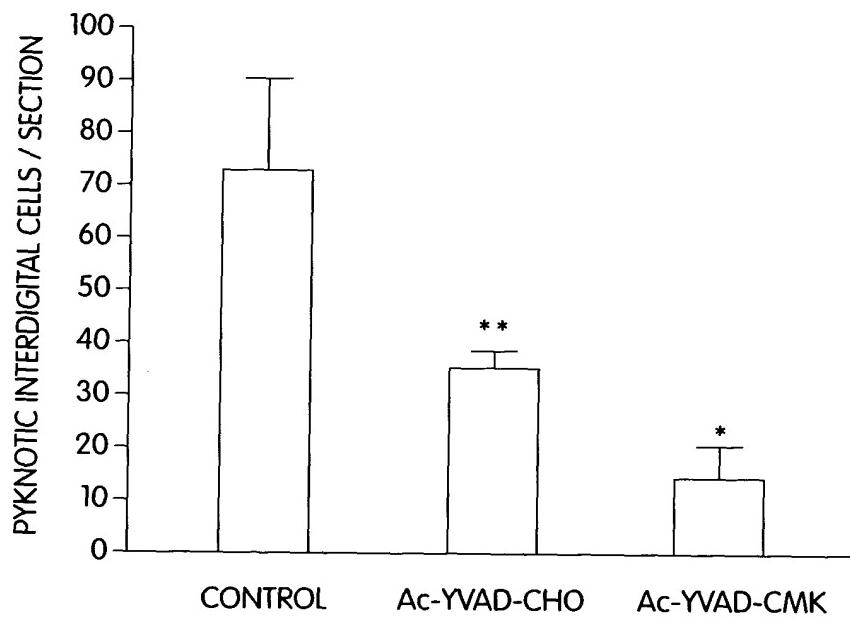


Fig. 14

0988474-E090-062201

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Fig. 15C



Fig. 15D



Fig. 15E



Fig. 15F

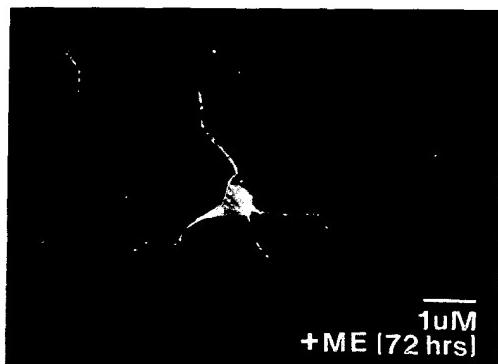


Fig. 15G